

DOCUMENT TYPE: Patent  
LANGUAGE: French  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
FR 2669338	A1	19920522	FR 1990-14519	19901121
FR 2669338	B1	19950303		
WO 9209632	A1	19920611	WO 1991-FR917	19911120
W: CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
EP 564477	A1	19931013	EP 1992-900187	19911120
EP 564477	B1	19981104		
R: AT, BE, CH, DE, GB, LI, LU, NL				
AT 172983	T	19981115	AT 1992-900187	19911120
FR 1990-14519 A 19901121				
WO 1991-FR917 W 19911120				

PRIORITY APPLN. INFO.:  
AB

Peptide fragments are disclosed which are derived from the external protein of FIV. Also disclosed are antibodies to the peptide fragments and use of the fragments and the antibodies (alone or conjugated to other substances, e.g. glucose oxidase) for therapeutics and diagnostics. Five specific peptide sequences are claimed. Also claimed is a model for evaluating the efficacy of immunoconjugates. The peptides were used in an ELISA format to test serum samples from FIV-infected and noninfected cats. Results of use of the peptides conjugated to albumin or hemocyanin as immunogens is also reported, as are the preparation and testing of an anti-peptide antibody immunoconjugate with glucose oxidase.

L13 ANSWER 11 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 1992-424420 ZCAPLUS Full-text  
DOCUMENT NUMBER: 117-24420

TITLE: Localization of three epitopes of the env protein of feline immunodeficiency virus

AUTHOR(S): Avrameas, Alexandre; Guillet, Jean Gerard; Chouchane, A. Donny; Morailon, Anne; Sonigo, Pierre; Strosberg, A. Donny

CORPORATE SOURCE: Inst. Cochin Genet. Mol., Univ. Paris VII, Paris, Fr.  
SOURCE: Molecular Immunology (1992), 29(5), 565-72  
CODEN: MOIMD5; ISSN: 0161-5890

DOCUMENT TYPE: Journal  
LANGUAGE: English

AB The envelope protein of the feline immunodeficiency virus (FIV) was analyzed using several epitope prediction programs based on profiles of hydrophilicity, antigenicity, and probability of residues lying on the protein surface. Tentative homologues with the immunodominant epitope sites in simian virus (SIV) or human immunodeficiency virus (HIV) such as the V3 loop, the site of cleavage between surface envelope protein (SU) and transmembrane envelope protein (TM), and sites of N-glycosylation were thus identified. Five peptides corresponding to potential epitopes were synthesized. Four out of 5 peptides (p99, p100, p101, p103) were from the FIV surface envelope protein (SU). The last one (p102) was from the FIV transmembrane envelope protein TM. Three of these peptides (p99, p100, and p102) were recognized in ELISA by almost all the sera from infected cats. The peptide from TM (p102) was recognized by sera from both naturally infected and inoculated cats, whereas peptide p99 and p100 (from SU) were recognized mainly by sera from naturally infected cats. Thus, peptides p99 and p100 from SU and p102 from TM constitute epitopes on the FIV env protein.

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DICTIONARY FILE UPDATES: 2 JUL 2007 HIGHEST RN 940883-34-1

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FILE LAST UPDATED: 2 Jul 2007 (20070702/ED)

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=> d ibib abs hitind L11 1-8.

L11 ANSWER 1 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:1099900 ZCAPLUS Full-text

DOCUMENT NUMBER: 146:121082

TITLE: The 160-kilobase genome of the bacterial endosymbiont

AUTHOR (S):

Carsonella  
Nakabachi, Atsushi; Yamashita, Atsushi; Toh,  
Hideohiro; Ishikawa, Hajime; Dunbar, Helen E.; Moran,  
Nancy A.; Hattori, Masahira  
Environmental Molecular Biology, RIKEN, Wako, Saitama,  
351-0198, Japan  
Science (Washington, DC, United States) (2006),  
314(5797), 267

CORPORATE SOURCE:

Science (Washington, DC, United States) (2006),  
314(5797), 267

SOURCE:

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER:  
American Association for the Advancement of Science

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB

Previous studies have suggested that the minimal cellular genome could be as  
sequence of the psyllid symbiont Carsonella ruddii, which consists of a  
circular chromosome of 159,662 base pairs, averaging 16.5% GC content. It is  
the smallest and most AT-rich bacterial genome characterized to date. The  
genome has a high coding d. (97%) with many overlapping genes and reduced gene  
length. Genes for translation and amino acid biosynthesis are relatively well  
represented, but numerous genes considered essential for life are missing,  
suggesting that Carsonella may have achieved organelle-like status.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 10

IT 915062-79-2 915062-80-5 915062-81-6 915062-82-7 915062-83-8  
915062-84-9 915062-85-0 915062-86-1 915062-87-2 915062-88-3  
915062-89-4 915062-90-7 915062-91-8 915062-92-9 915062-93-0  
915062-94-1 915062-95-2 915062-96-3 915062-97-4 915062-98-5  
915062-99-6 915063-00-2 915063-01-3 915063-02-4 915063-03-5  
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915064-09-4  
GTPase (Carsonella ruddii strain PV) 915064-10-7  
915064-11-8 915064-12-9 915064-13-0 915064-14-1 915064-15-2  
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915064-41-4 915064-42-5 915064-43-6 915064-44-7 915064-45-8  
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915064-56-1 915064-57-2 915064-58-3 915064-59-4

915064-60-7  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
 (amino acid sequence; complete sequence of 160-kilobase genome of bacterial endosymbiont Carsonella ruddii)  
 REFERENCE COUNT: 5  
 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 2 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN  
 ACCESSION NUMBER: 2006:769164 ZCAPLUS Full-text  
 DOCUMENT NUMBER: 145:224845  
 TITLE: Anti-angiogenic peptides and methods of use thereof  
 INVENTOR(S): Rastelli, Luca; Landin, Judith; Malyankar, Uriel; Kitson, Richard; Corso, Melissa; Brunson, Kenneth  
 PATENT ASSIGNEE(S): USA  
 SOURCE: U.S. Pat. Appl. Publ., 48pp., Cont.-in-part of PCT/US05/36959.  
 CODEN: USXACO  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 2  
 PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE  
 US 2006172941 A1 20060803 US 2006-127849 20060109  
 WO 2006044614 A2 20060427 WO 2005-US36959 20051014  
 WO 2006044614 A3 20060810  
 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EG, ES, FI, GB, GE, GH, GM, GR, GU, ID, IL, IN, IS, JP, KE, KM, KP, KR, KZ, LA, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, NZ, NC, NG, NI, NO, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW  
 RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BI, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
 PRIORITY APPLN. INFO.:  
 US 2004-618273P P 20041014  
 WO 2005-US36959 A2 20051014  
 OTHER SOURCE(S): MARPAT 145:224845  
 AB Anti-angiogenic peptides that inhibit activation or proliferation of endothelial cells are disclosed. Such peptides may be used to inhibit VEGF binding to the VEGFR2 receptor (also known as the kinase domain receptor or KDR) and bFGF binding to its receptor. Such peptides may also be used to inhibit, VEGF, bFGF, or integrin activation of endothelial cells in angiogenesis-associated diseases such as cancer, leukemia, multiple myeloma, inflammatory diseases, eye diseases and skin disorders.  
 INCL 514012000: 530350000  
 CC 1-6 (Pharmacology)  
 Section cross-reference(s): 63  
 IT 111793-75-0 143740-07-2 144095-01-2 147236-19-9 176254-16-3  
 184703-88-6 190894-91-8 205117-83-5 211106-37-5 213617-98-2  
 220334-13-4 243961-51-5 247111-51-9 268214-27-3 268539-66-8  
 272121-15-0 353483-40-6 359636-54-7 364618-18-8 364618-24-6  
 364618-25-7 364618-26-8 492444-99-2 494228-18-1 498573-01-6  
 502719-76-8 573664-51-4 875516-71-5 875517-64-9 875575-92-9  
 884508-78-5 884508-79-6 884508-80-9 884508-81-0 884508-82-1

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 904743-66-4D, biotinylated 904743-67-5 904743-68-6 904743-69-7  
 904743-71-1 904743-72-2 905438-56-4  
 RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
 (anti-angiogenic peptides and methods of use thereof)

L11 ANSWER 3 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN  
 ACCESSION NUMBER: 2006:647420 ZCAPLUS Full-text  
 DOCUMENT NUMBER: 145:77446  
 TITLE: Complete genome sequence of the chlorarachniophyte nucleomorph: Nature's smallest nucleus  
 AUTHOR(S): Gilson, Paul R.; Su, Vanessa; Slamovits, Claudio H.; Reith, Michael E.; Keeling, Patrick J.; McFadden, Geoffrey I.  
 CORPORATE SOURCE: Infection and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, 3050, Australia  
 SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2006), 103(25), 9566-9571  
 CODEN: PNASAG; ISSN: 0027-8424  
 PUBLISHER: National Academy of Sciences  
 DOCUMENT TYPE: Journal  
 LANGUAGE: English  
 AB The introduction of plastids into different heterotrophic protists created lineages of algae that diversified explosively, proliferated in marine and freshwater environments, and radically altered the biosphere. The origins of these secondary plastids are usually inferred from the presence of adnl. plastid membranes. However, two examples provide unique snapshots of secondary-endosymbiosis-in-action, because they retain a vestige of the endosymbiont nucleus known as the nucleomorph. These are chlorarachniophytes and cryptomonads, which acquired their plastids from a green and red alga resp. To allow comparisons between them, the nucleomorph genome from the chlorarachniophyte Bigelowiella natans was sequenced: at a mere 373,000 bp and with only 331 genes, the smallest nuclear genome known and a model for extreme reduction. The genome is eukaryotic in nature, with 3 linear chromosomes containing densely packed genes with numerous overlaps. The genome is replete with 852 introns, but these are the smallest introns known, being only 18, 19, 20, or 21 nt in length. These pygmy introns are shown to be miniaturized versions of normal-sized introns present in the endosymbiont at the time of capture. Seventeen nucleomorph genes encode proteins that function in the plastid. The other nucleomorph genes are housekeeping entities, presumably underpinning maintenance and expression of these plastid proteins. Chlorarachniophyte plastids are thus serviced by 3 different genomes (plastid, nucleomorph, and host nucleus) requiring remarkable coordination and targeting. Although originating by 2 independent endosymbioses, chlorarachniophyte and cryptomonad nucleomorph genomes have converged upon remarkably similar architectures but differ in many mol. details that reflect 2 distinct trajectories to hypercompaction and reduction. The B. natans nucleomorph genome sequence is deposited in GenBank/EMBL/DBJ under accession nos. DQ158856-DQ158858.  
 CC 3-3 (Biochemical Genetics)  
 Section cross-reference(s): 6, 10

IT 892535-81-8 892535-82-9 892535-83-0 892535-84-1 892535-85-2  
892535-86-3 892535-87-4 892535-88-5 892535-89-6 892535-90-9  
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892538-17-9 892538-18-0 892538-19-1 892538-20-2 892538-21-3

LI1 ANSWER 4 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 2006:412218 ZCAPLUS Full-text  
DOCUMENT NUMBER: 144:383037  
TITLE: Pathogenomic sequence analysis of *Bacillus cereus* and

*Bacillus thuringiensis* isolates closely related to  
*Bacillus anthracis*  
Han, Cliff S.; Xie, Gary; Challacombe, Jean F.;  
Altherr, Michael R.; Bhotika, Smriti S.; Bruce, David;  
Campbell, Connie S.; Campbell, Mary L.; Chen, Jin;  
Chertkov, Olga; Cleland, Cathy; Dimitrijevic, Mira;  
Doggett, Norman A.; Fawcett, John J.; Glavina, Tijana;  
Goodwin, Lynne A.; Hill, Karen K.; Hitchcock, Penny;  
Jackson, Paul J.; Keim, Paul; Kewalramani, Avinash  
Ramesh; Longmire, Jon; Lucas, Susan; Malfatti,  
Stephanie; McMurry, Kim; Meincke, Linda J.; Misra,  
Monica; Moseman, Bernice L.; Mundt, Mark; Munk, A.  
Christine; Okinaka, Richard T.; Parson-Quintana, B.;  
Reilly, Lee Philip; Richardson, Paul; Robinson, Donna  
L.; Rubin, Eddy; Saunders, Elizabeth; Tapia, Roxanne;  
Tesmer, Judith G.; Thayer, Nina; Thompson, Linda S.;  
Tice, Hope; Ticknor, Lawrence O.; Wills, Patti L.;  
Brettin, Thomas S.; Gilna, Paul  
DOE Joint Genome Institute Los Alamos National  
Laboratory, Los Alamos, NM, 87545, USA  
Journal of Bacteriology (2006), 188(9), 3382-3390  
CODEN: JDBAAY; ISSN: 0021-9139  
American Society for Microbiology  
Journal  
English  
AB *Bacillus anthracis*, *Bacillus cereus*, and *Bacillus thuringiensis* are closely  
related gram-pos., spore-forming bacteria of the *B. cereus sensu lato* group.  
While independently derived strains of *B. anthracis* reveal conspicuous  
sequence homogeneity, environmental isolates of *B. cereus* and *B. thuringiensis*  
exhibit extensive genetic diversity. This report describes the sequencing and  
comparative anal. of the genomes of two members of the *B. cereus* group, *B.*  
*thuringiensis* 97-27 subsp. *konkukian* serotype H34, isolated from a necrotic  
human wound, and *B. cereus* E33L, which was isolated from a swab of a zebra  
carcass in Namibia. These two strains, when analyzed by amplified fragment  
length polymorphism within a collection of over 300 of *B. cereus*, *B.*  
*thuringiensis*, and *B. anthracis* isolates, appear closely related to *B.*  
*anthracis*. The *B. cereus* E33L isolate appears to be the nearest relative to  
*B. anthracis* identified thus far. Whole-genome sequencing of *B. thuringiensis*  
97-27 and *B. cereus* E33L was undertaken to identify shared and unique genes  
among these isolates in comparison to the genomes of pathogenic strains *B.*  
*anthracis* Ames and *B. cereus* G9241 and nonpathogenic strains *B. cereus* ATCC  
10987 and *B. cereus* ATCC 14579. Comparison of these genomes revealed  
differences in terms of virulence, metabolic competence, structural  
components, and regulatory mechanisms. The *B. thuringiensis* 97-27 and its  
plasmid pBT9727 sequences are deposited in GenBank/EMBL/DBJ under accession  
nos. AE017355 and CP000047, and the *B. cereus* E33L and five plasmids sequences  
are deposited under CP000001 and CP000040-CP000044. [This abstract record is  
one of two records for this document necessitated by the large number of index  
entries required to fully index the document and publication system  
constraints.]  
CC 3-3 (Biochemical Genetics)  
Section cross-reference(s): 6, 10, 14  
IT 883428-51-1 883428-52-2 883428-53-3 883428-54-4 883428-55-5,  
Protein (plasmid pE33L466 87-amino acid) 883428-56-6, Thioresoxin  
(plasmid pE33L466) 883428-57-7 883428-58-8 883428-59-9  
883428-60-2, Protein (plasmid pE33L466 78-amino acid) 883428-61-3,  
Protein (plasmid pE33L466 82-amino acid) 883428-62-4, Protein (plasmid  
pE33L466 73-amino acid) 883428-63-5 883428-64-6, Transposase (plasmid  
pE33L466 gene tnp) 883428-65-7, Transposase (plasmid pE33L466 gene tnp)  
883428-66-8 883428-67-9 883428-68-0, Protein (plasmid pE33L466



YU, ZA, ZM, ZW  
 RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BU, CF, CG, CI, CN, GA, GN, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
 CA 2583399 A1 20060427 CA 2005-2583399 20051014  
 US 2006172941 A1 20060803 US 2006-327849 20060109  
 PRIORITY APPLN. INFO.: US 2004-618273P P 20041014  
 WO 2005-US36959 W 20051014  
 OTHER SOURCE(S): MARPAT 144:440088  
 AB Anti-angiogenic peptides that inhibit activation or proliferation of endothelial cells are disclosed. Such peptides may be used to inhibit VEGF binding to the VEGFR2 receptor (also known as the kinase domain receptor or KDR) and bFGF binding to its receptor. Such peptides may also be used to inhibit VEGF, bFGF, or integrin activation of endothelial cells in angiogenesis-associated diseases such as cancer, leukemia, multiple myeloma, inflammatory diseases, eye diseases and skin disorders.  
 CC 63-6 (Pharmaceuticals)  
 IT Section cross-reference(s): 1 884508-78-5 884508-79-6 884508-80-9  
 884508-81-0 884508-82-1 884508-83-2 884508-84-3 884508-85-4  
 884508-86-5 884508-87-6 884508-88-7 884508-89-8 884508-90-1  
 884508-91-2 884508-92-3 884508-93-4 884508-94-5 884508-95-6  
 884508-96-7 884508-99-6 884551-00-2 884551-01-3  
 884551-02-4  
 RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
 (anti-angiogenic peptides and methods of use thereof)

L11 ANSWER 6 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN  
 ACCESSION NUMBER: 2005-603637 ZCAPLUS Full-text  
 DOCUMENT NUMBER: 143:91812  
 TITLE: The genome of the kinetoplastid parasite, Leishmania major

AUTHOR(S): Ivens, Alasdair C.; Peacock, Christopher S.; Worthey, Elizabeth A.; Murphy, Lee; Aggarwal, Gautam; Berriman, Matthew; Sisk, Ellen; Rajandream, Marie-Adele; Adiem, Ellen; Aert, Rita; Anupama, Atashi; Apostolou, Zina; Attipoe, Philip; Bason, Nathalie; Bauser, Christopher; Beck, Alfred; Beverley, Stephen M.; Blanchettin, Gabriella; Borzym, Katja; Bothe, Gordana; Bruschi, Carlo V.; Collins, Matt; Cadag, Eithon; Clarlioni, Laura; Clayton, Christine; Coulson, Richard M. R.; Cronin, Ann; Cruz, Angela K.; Davies, Robert M.; De Gaudenzi, Javier; Dobson, Deborah E.; Dueterhoeft, Andreas; Fazelina, Ghulam; Fosker, Nigel; Frasch, Alberto Carlos; Fraser, Audrey; Fuchs, Monika; Gabel, Claudia; Goble, Arlette; Goffeau, Andre; Harris, David; Herts-Fowler, Christiane; Hilbert, Helmut; Horn, David; Huang, Yiting; Klages, Sven; Knights, Andrew; Kube, Michael; Larke, Natasha; Litvin, Lyudmila; Lord, Angela; Louie, Tin; Marra, Marco; Masny, David; Matthews, Keith; Michaeli, Shulamit; Mottram, Jeremy C.; Mueller-Auer, Silke; Munden, Heather; Nelson, Siri; Norbertczak, Halina; Oliver, Karen; O'Neill, Susan; Pentony, Martin; Pohl, Thomas M.; Price, Claire; Purnelle, Benedicte; Quail, Michael A.; Rabinowitsch, Ester; Reinhardt, Richard; Rieger, Michael; Rinta, Joel; Robben, Johan; Robertson, Laura;

Ruiz, Jeronimo C.; Rutter, Simon; Saunders, David; Schaefer, Melanie; Schein, Jacques; Schwartz, David C.; Seeger, Kathy; Seyler, Amber; Sharp, Sarah; Shin, Heesun; Sivam, Dhileep; Squares, Rob; Squares, Steve; Tosato, Valentina; Vogt, Christy; Volckaert, Guido; Wambutt, Rolf; Warren, Tim; Wedler, Holger; Woodward, John; Zhou, Shiguo; Zimmermann, Wolfgang; Smith, Deborah F.; Blackwell, Jenefer M.; Stuart, Kenneth D.; Barrall, Bart; Myler, Peter J.  
 Wellcome Trust Genome Campus, Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK  
 Science (Washington, DC, United States) (2005), 309(5733), 436-442  
 CODEN: SCIEAS; ISSN: 0036-8075  
 American Association for the Advancement of Science  
 Journal  
 English  
 AB Leishmania species cause a spectrum of human diseases in tropical and subtropical regions of the world. The 36 chromosomes of the 32.8-megabase haploid genome of Leishmania major (Friedlin strain) were sequenced and 911 RNA genes, 39 pseudogenes, and 8272 protein-coding genes were predicted, of which 36% can be ascribed a putative function. These include genes involved in host-pathogen interactions, such as proteolytic enzymes, and extensive machinery for synthesis of complex surface glycoconjugates. The organization of protein-coding genes into long, strand-specific, polycistronic clusters and lack of general transcription factors in the L. major, Trypanosoma brucei, and Trypanosoma cruzi (Trityp) genomes suggest that the mechanisms regulating RNA polymerase II-directed transcription are distinct from those operating in other eukaryotes, although the trypanosomatids appear capable of chromatin remodeling. Abundant RNA-binding proteins are encoded in the Trityp genomes, consistent with active posttranscriptional regulation of gene expression. The genome sequence is deposited in GenBank/EMBL/DBJ under accession nos. CT005244-CT005272, AL389894, AL39794, CP000078-CP000081, AE001274, and NC\_004916. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.]

CC 3-3 (Biochemical Genetics) 6, 10  
 IT Section cross-reference(s): 6, 10  
 856545-34-1 856545-35-2 856545-36-3 856545-37-4 856545-38-5  
 856545-39-6 856545-40-9 856545-41-0 856545-42-1 856545-43-2  
 856545-44-3 856545-45-4 856545-46-5 856545-47-6 856545-48-7  
 856545-49-8 856545-50-1 856545-51-2 856545-52-3 856545-53-4  
 856545-54-5 856545-55-6 856545-56-7 856545-57-8 856545-58-9  
 856545-59-0 856545-60-3 856545-61-4 856545-62-5 856545-63-6  
 856545-64-7 856545-65-8 856545-66-9 856545-67-0 856545-68-1  
 856545-69-2 856545-70-5 856545-71-6 856545-72-7 856545-73-8  
 856545-74-9 856545-75-0 856545-76-1 856545-77-2 856545-78-3  
 856545-79-4 856545-80-7 856545-81-8 856545-82-9  
 856545-83-0 856545-84-1 856545-85-2 856545-86-3 856545-87-4  
 856545-88-5 856545-89-6 856545-90-9 856545-91-0 856545-92-1  
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 856546-03-7 856546-04-8 856546-05-9 856546-06-0 856546-07-1  
 856546-08-2 856546-09-3 856546-10-6 856546-11-7 856546-12-8  
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856546-93-5 856546-94-6 856546-95-7 856546-96-8 856546-97-9  
856546-98-0 856546-99-1

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(amino acid sequence; genome sequence of Leishmania major)  
(140:194469)

REFERENCE COUNT: 52  
THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS  
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 7 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 2004:155816 ZCAPLUS Full-text  
DOCUMENT NUMBER: 140:194469

TITLE: Nucleic acids and encoded proteins associated with  
plants and their uses for plant improvement  
Liu, Jingdong; Zhou, Yihua; Kovacic, David K.; Screen,  
Steven E.; Tabaska, Jack E.; Cao, Yongwei

INVENTOR(S): USA  
PATENT ASSIGNEE(S): U.S. Pat. Appl. Publ., 15 pp., Cont. -in-part of U.S.  
SOURCE: Ser. No. 985,678, abandoned.  
CODENT: USXXCO  
PARENT: Patent

DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 76

PATENT INFORMATION:  
PATENT NO. KIND DATE APPLICATION NO. DATE  
US 2004034888 A1 20040219 US 2003-425114 20030428  
US 2004034888 A1 20040219 US 2003-425114 20030428  
PRIORITY APPLN. INFO.: US 1999-304517 B1 19990506  
US 2001-985678 B2 20011105  
US 2003-425114 A 20030428

AB This invention provides 36,564 polynucleotide sequences isolated from cDNA  
libraries generated from various plants, including Zea mays, Glycine max,  
Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum  
aestivum, Eugenia gracilis, Chlorella vulgaris, Schizochytrium aggregatum,  
Brassica napus, Gossypium hirsutum, Cucumis sativus, Lillium asiatic, Sorghum  
bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum. The  
open reading frame in each polynucleotide sequence is identified by a  
combination of predictive and homol.-based methods. Functions of polypeptides  
encoded by the polynucleotides sequences are determined using a hierarchical  
classification tool, termed FunCAR, for Functional Categories Annotation Tool.  
Sequences useful for producing transgenic plants having improved biol.  
properties are identified from their FunCAR annotations. [This abstract  
record is one of 19 records for this document necessitated by the large number  
of index entries required to fully index the document and publication system  
constraints.]

IC ICN A01H001-00  
ICS C12N015-82; C07H021-04; C07K014-415; C12N009-24  
INCL 800290000; 530370000; 536023600; 435200000  
CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 6, 11  
IT 61661-20-7 61661-21-8 61661-22-9 61661-23-0 61661-24-1  
61661-25-2 61661-26-3 61661-27-4 61661-28-5 61661-29-6  
61661-30-9 61661-31-0 61661-32-1 61661-33-2 61661-34-3  
61661-35-4 61661-36-5 61661-37-6 61661-38-7 61661-39-8  
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61663-56-5 61663-57-6 61663-58-7 61663-59-8 61663-60-1  
61663-61-2 61663-62-3 61663-63-4

RL: BSU (Biological study, unclassified); BVU (Biological use,  
unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; nucleic acids and encoded proteins associated with  
plants and their uses for plant improvement)

L11 ANSWER 8 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN  
ACCESSION NUMBER: 2003:796119 ZCAPLUS Full-text  
DOCUMENT NUMBER: 139:312392

TITLE: Biological affinity-based drug delivery systems  
INVENTOR(S): Panitch, Alyssa; Seal, Brandon  
PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 33 pp.

CODEN: USXXCO

DOCUMENT TYPE:

LANGUAGE: Patent

FAMILY ACC. NUM. COUNT: 1 English

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

US 2003190364 A1 20031009 US 2003-405339 20030401

WO 2003084481 A2 20031016 WO 2003-US9887 20030401

WO 2003084481 A3 20040401

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, GR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, MG, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GN, GW, HT, IL, LU, MC, NL, PT, RO, SE, SI, SK, TR, AU 2003260668 A1 20031020 AU 2003-260668 20030401

PRIORITY APPLN. INFO.: US 2002-369568P P 20020401 WO 2003-US9887 W 20030401

AB The present invention provides compns. for drug delivery, comprising a polymer network; a plurality of polysaccharide binding (PB) polypeptides, wherein the plurality of PB polypeptides are covalently bound to the polymer network, but wherein the PB polypeptides do not serve to covalently cross-link the polymer network; and neg. charged polysaccharides non-covalently bound to the plurality of PB polypeptides; as well as methods for making and using the compns.

IC ICM A61K038-17

INCL ICS A61K031-727; A61K009-14; A61K031-737; A61K031-728

CC 63-5 (Pharmaceuticals)

IT 9003-16-1, Polyfumaric acid 25189-55-3, Poly(n-isopropylacrylamide) 117609-40-2 145123-91-7 176502-05-9 188642-14-0 191936-91-1 220408-24-2 227199-94-2 227199-95-3 227199-96-4 227199-97-5 227199-98-6 227199-99-7 287393-83-2 287393-83-3 373389-48-1 393153-52-1 395069-86-0 406482-85-7 496958-05-5 500724-83-4 500724-84-5 500724-85-6 500724-86-7 500724-87-8 500724-88-9 500724-94-7 57314-86-0 610317-75-4 610317-76-5 610317-77-6 610317-78-7 610317-79-8 610317-80-1 610317-81-2 610317-82-3 610317-83-4 610317-84-5 610317-85-6 610317-86-7 610317-87-8 610317-88-9 610317-89-0 610317-90-3 610317-91-4 610317-92-5 610317-93-6 610317-94-7 610317-95-8 610317-96-9 610323-96-1 610323-97-2 610323-98-3 610323-99-4

RL: PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (biol. affinity-based drug delivery systems)



FILE REGISTRY

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 2 JUL 2007 HIGHEST RN 940883-34-1  
DICTIONARY FILE UPDATES: 2 JUL 2007 HIGHEST RN 940883-34-1

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<http://www.cas.org/support/stngen/stdoc/properties.html>

FILE ZCAPLUS

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FILE LAST UPDATED: 2 Jul 2007 (20070702/ED)

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FILE STNGUIDE

FILE CONTAINS CURRENT INFORMATION.  
LAST RELOADED: Jun 29, 2007 (20070629/UP).

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COST IN U.S. DOLLARS	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

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STRUCTURE FILE UPDATES: 1 JUL 2007 HIGHEST RN 940612-32-8  
DICTIONARY FILE UPDATES: 1 JUL 2007 HIGHEST RN 940612-32-8

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH December 2, 2006

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conducting SmartSELECT searches.

REGISTRY includes numerically searchable data for experimental and  
predicted properties as well as tags indicating availability of  
experimental property data in the original document. For information  
on property searching in REGISTRY, refer to:

<http://www.cas.org/support/stngen/stndoc/properties.html>

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The following are valid formats:

Substance information can be displayed by requesting individual  
fields or predefined formats. The predefined substance formats  
are: (RN = CAS Registry Number)

REG	- RN
SAM	- Index Name, MF, and structure - no RN
FIDE	- All substance data, except sequence data
IDE	- FIDE, but only 50 names
SQIDE	- IDE, plus sequence data

SQIDE3 - Same as SQIDE, but 3-letter amino acid codes are used  
SQD - Protein sequence data, includes RN  
SQD3 - Same as SQD, but 3-letter amino acid codes are used  
SQN - Protein sequence name information, includes RN  
  
CALC - Table of calculated properties  
EPROP - Table of experimental properties  
PROP - EPROP and CALC

Any CA File format may be combined with any substance format to obtain CA references citing the substance. The substance formats must be cited first. The CA File predefined formats are:

ABS -- Abstract  
APPS -- Application and Priority Information  
BIB -- CA Accession Number, plus Bibliographic Data  
CAN -- CA Accession Number  
CBIB -- CA Accession Number, plus Bibliographic Data (compressed)  
IND -- Index Data  
IPC -- International Patent Classification  
PATS -- PI, SO  
STD -- BIB, IPC, and NCL  
  
IABS -- ABS, indented, with text labels  
IBIB -- BIB, indented, with text labels  
ISTD -- STD format, indented  
  
OBIB ----- AN, plus Bibliographic Data (original)  
OIBIB ----- OBIB, indented with text labels  
  
SBIB ----- BIB, no citations  
SIBIB ----- IBIB, no citations

The ALL format gives FIDE BIB ABS IND RE, plus sequence data when it is available.

The MAX format is the same as ALL.

The IALL format is the same as ALL with BIB ABS and IND indented, with text labels.

For additional information, please consult the following help messages:

HELP DFIELDS -- To see a complete list of individual display fields.  
HELP FORMATS -- To see detailed descriptions of the predefined formats.  
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CN   Protein (Oryza sativa japonica strain Nipponbare gene Os07g0164800)  (CA
      INDEX NAME)
OTHER NAMES:
CN   GenBank BAF20877
CN   GenBank BAF20877 (Translated from: GenBank AP008213)
FS   PROTEIN SEQUENCE
SQL  275
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201 DLQAKKEDIL RQLKEQLKEE LEGGKSKNAI EEKPAQTLEK GIEHNKPIEE

251 KPAETVEGSR ECKNNEKEET HVAAA

HITS AT: 102-119

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR GenBank

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 2 OF 6 REGISTRY COPYRIGHT 2007 ACS on STN

RN 846538-32-7 REGISTRY

CN L-Arginine, L-cysteinylglycyl-L-alanyl-L-tyrosyl-L- $\alpha$ -aspartyl-L-leucyl-L-arginyl-L-arginyl-L-arginyl-L- $\alpha$ -glutamyl-L-arginyl-L-glutamyl-L-seryl-L-arginyl-L-leucyl-L-arginyl-L-arginyl-L- $\alpha$ -glutamyl-L-arginyl-L-glutamyl-L-seryl- (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 23

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HITS AT: 6-23

MF C119 H211 N55 O35 S

SR CA

LC STN Files: CA, CAPLUS

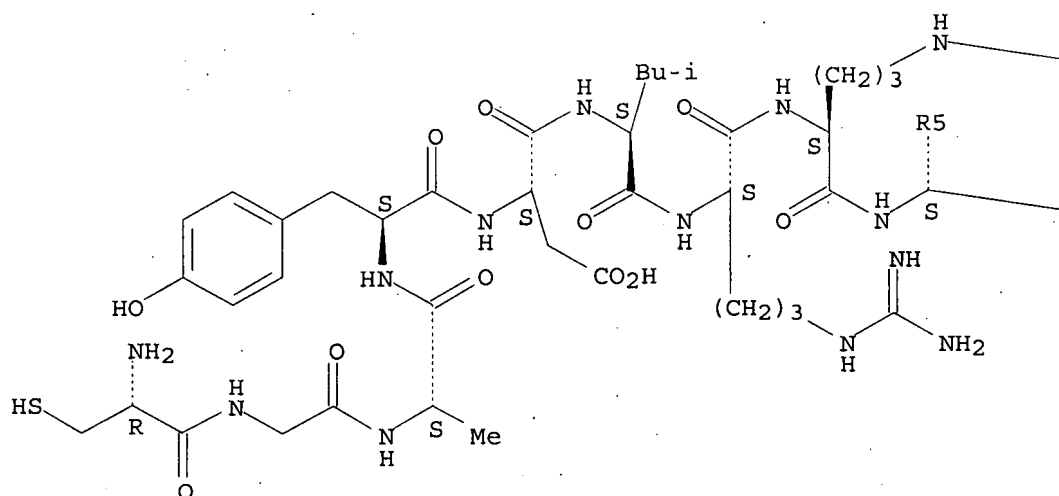
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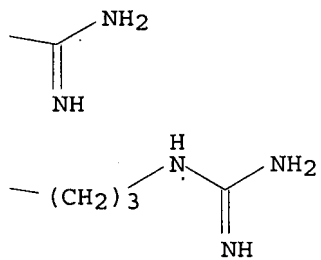
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Absolute stereochemistry.

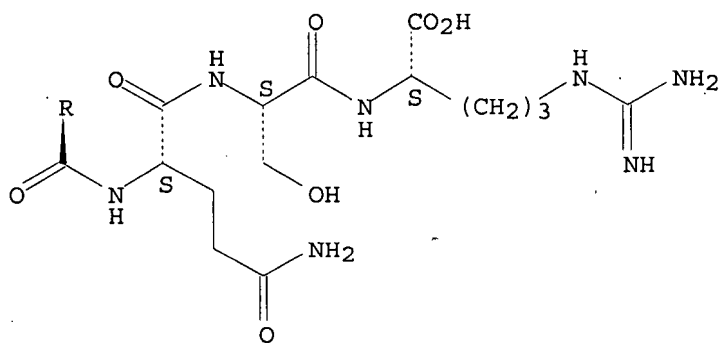
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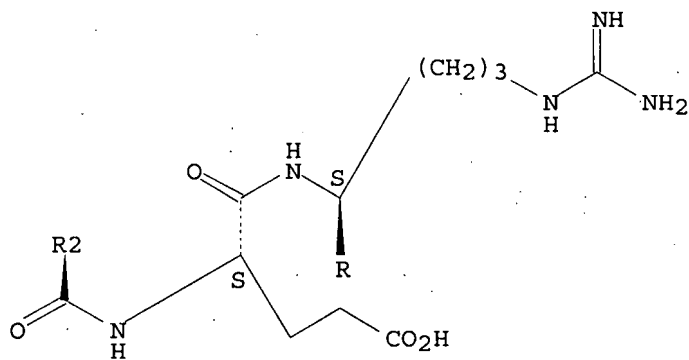
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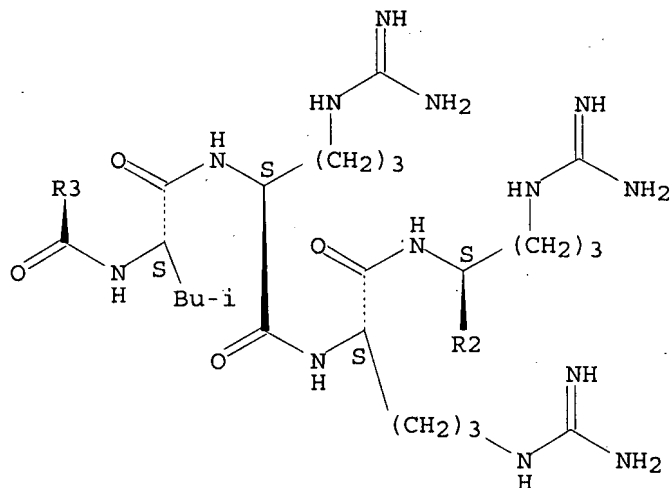
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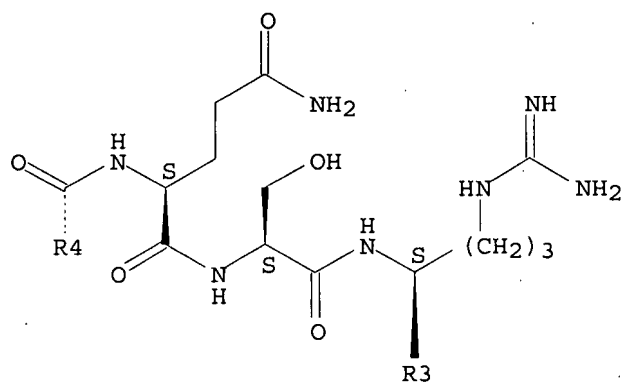
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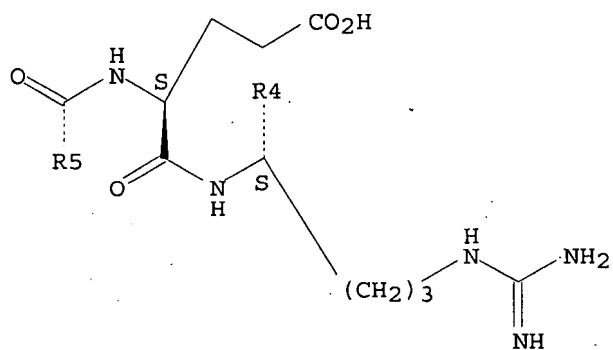
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PAGE 5-A



PAGE 6-A



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CN L-Arginine, glycyL-L-alanyl-L-tyrosyl-L- $\alpha$ -aspartyl-L-leucyl-L-  
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L-arginyL-L-glutaminyL-L-seryl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2: PN: WO2005016960 SEQID: 2 claimed sequence

CN 7: PN: FR2858772 SEQID: 7 claimed sequence

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 22

PATENT ANNOTATIONS (PNTE):

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Source | Reference

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Not Given | FR2858772  
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          | WO2005016960  
          | claimed SEQID  
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MF C116 H206 N54 O34

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

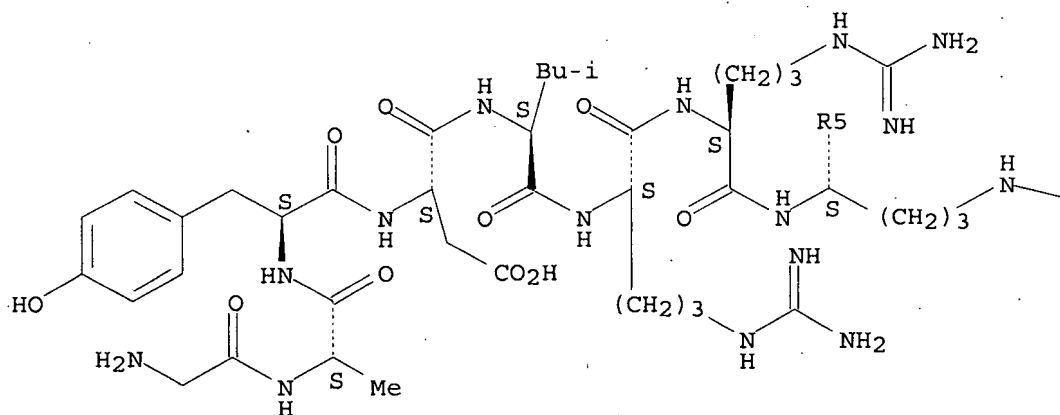
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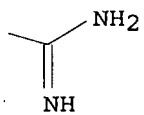
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Absolute stereochemistry.

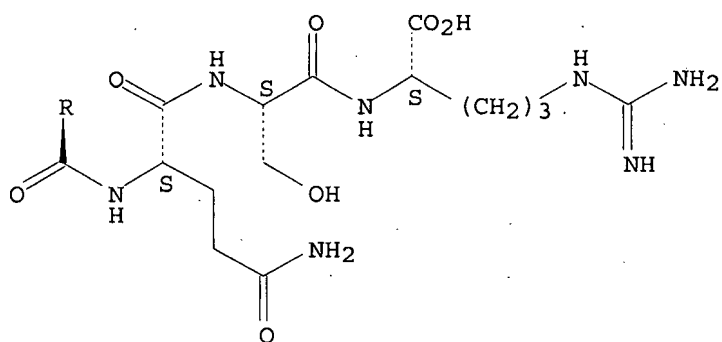
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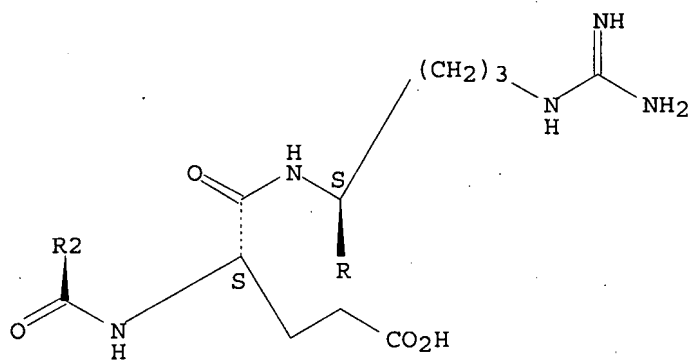
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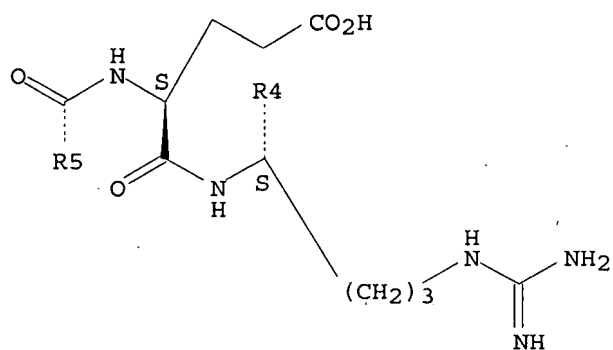
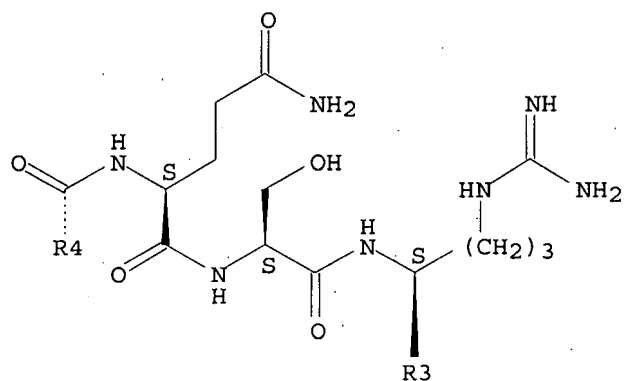
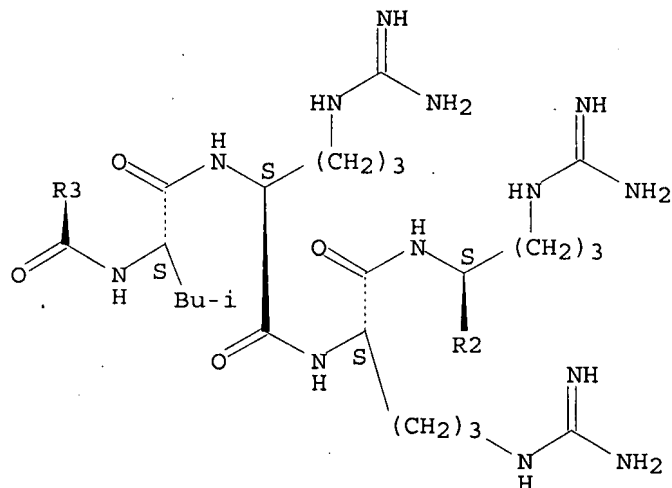
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PAGE 3-A







3 REFERENCES IN FILE CA (1907 TO DATE)  
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 3 REFERENCES IN FILE CAPLUS (1907 TO DATE)

CN Protein (Oryza sativa clone PAT\_MRT4530\_76304C.1.pep fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3777: PN: US20040123343 SEQID: 178781 claimed protein.  
FS PROTEIN SEQUENCE  
SQL 275

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	US2004123343 claimed SEQID 178781

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251 KPAETVEGSR ECKNNEKEET HVAAA

HITS AT: 102-119

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS  
DT.CA Caplus document type: Patent  
RL.P Roles from patents: BIOL (Biological study); PRP (Properties); USES (Uses)  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 5 OF 6 REGISTRY COPYRIGHT 2007 ACS on STN  
RN 671322-72-8 REGISTRY  
CN Transcription-associated protein (Glycine max clone PAT\_MRT3847\_31785C.1.pep fragment) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 2140: PN: US20040031072 SEQID: 210140 claimed protein  
FS PROTEIN SEQUENCE  
SQL 300

PATENT ANNOTATIONS (PNTE):

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Source	Reference
Not Given	US2004031072 claimed SEQID 210140

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51 TQCDPPHTAV PRNYIGENV S RKDKNKYLYT TLLELND SKE AVYGALDAW  
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151 RALDMDHRVE EAQKFWEIKI GSDLHSVPWQ LCHLMISVYY RNNMLQDLVK  
201 LFKGLEAFDR KPRDKSIIQK VANAYEVLGL VKEKERVLEK YNHLFTETGP  
251 TKRHKRNSFE AKKHVHPTKE KRHQKQSRKA SSEEKYKSEQ KDPKLDIGHI  
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HITS AT: 261-278

MF Unspecified  
CI MAN

SR CA  
LC STN Files: CA, CAPLUS  
DT.CA Caplus document type: Patent  
RL.P Roles from patents: BIOL (Biological study); PRP (Properties); USES  
(Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L2 ANSWER 6 OF 6 REGISTRY COPYRIGHT 2007 ACS on STN  
RN 486859-91-0 REGISTRY  
CN GenBank BAC07421 (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank BAC07421 (Translated from: GenBank AP004267)  
FS PROTEIN SEQUENCE  
SQL 275

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201 DLQAKKEDIL RQLKEQLKEE LEGGKSKNAI EEKPAQTLEK GIEHNKPIEE  
251 KPAETVEGSR ECKNNEKEET HVAAA

HITS AT: 102-119

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified  
CI MAN  
SR GenBank

=> file hcaplus  
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FULL ESTIMATED COST

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FILE LAST UPDATED: 1 Jul 2007 (20070701/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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L4 7 L2  
=> d 14 1-7

L4 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2007 ACS on STN  
 AN 2007:163120 HCAPLUS  
 DN 146:178150  
 TI Curated genome annotation of *Oryza sativa* ssp. *japonica* and comparative genome analysis with *Arabidopsis thaliana*  
 AU Gojobori, Takashi  
 CS The Rice Annotation Project, Japan  
 SO Genome Research (2007), 17(2), 175-183  
 CODEN: GEREFS; ISSN: 1088-9051  
 PB Cold Spring Harbor Laboratory Press  
 DT Journal  
 LA English

L4 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2007 ACS on STN  
 AN 2005:876357 HCAPLUS  
 DN 143:353060  
 TI Novel human-derived cell-penetrating peptides for specific subcellular delivery of therapeutic biomolecules  
 AU De Coupade, Catherine; Fittipaldi, Antonio; Chagnas, Vanessa; Michel, Matthieu; Carlier, Sophie; Tasciotti, Ennio; Darmon, Audrey; Ravel, Denis; Kearsey, Jonathan; Giacca, Mauro; Cailler, Françoise  
 CS Diatos S.A., Paris, 75014, Fr.  
 SO Biochemical Journal (2005), 390(2), 407-418  
 CODEN: BIJOAK; ISSN: 0264-6021  
 PB Portland Press Ltd.  
 DT Journal  
 LA English

RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2007 ACS on STN  
 AN 2005:177899 HCAPLUS  
 DN 142:273964  
 TI Antibacterial composition, especially for controlling Gram-negative bacteria, comprising a peptide and a hydrophobic antibacterial agent  
 IN Arranz, Valerie  
 PA Diatos, Fr.  
 SO PCT Int. Appl., 53 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA French  
 FAN.CNT 3

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JP 2007502262 T 20070208 JP 2006-523036 20040813  
PRAI EP 2003-292030 A 20030814  
FR 2003-9962 A 20030814  
WO 2004-FR2142 W 20040813

L4 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2007 ACS on STN

AN 2005:161031 HCAPLUS

DN 142:266763

TI Peptide vectors facilitating intracellular or intranuclear delivery of  
drugs and their therapeutic use

IN Avrameas, Alexandre

PA Diatos, Fr.

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 3

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	WO 2005016960	A3	20050407		
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	EP 1512696	A1	20050309	EP 2003-292030	20030814
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	AU 2004265159	A1	20050224	AU 2004-265159	20040813
	CA 2535670	A1	20050224	CA 2004-2535670	20040813
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	US 2007042492	A1	20070222	US 2006-568108	20060213
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	FR 2003-9962	A	20030814		
	WO 2004-IB2936	W	20040813		

L4 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2007 ACS on STN

AN 2005:139996 HCAPLUS

DN 142:233277

TI Antibacterial composition, more particularly against Gram-negative  
bacteria, including a peptide and a hydrophobic antibacterial agent

IN Arranz, Valerie

PA Diatos, Fr.

SO Fr. Demande, 47 pp.

CODEN: FRXXBL

DT Patent

LA French

FAN.CNT 3

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RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2535745	A1	20050303	CA 2004-2535745	20040813
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK				

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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK				

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FILE 'REGISTRY' ENTERED AT 11:19:18 ON 02 JUL 2007

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L2 6 S [AILMFWVYGSTCPNQDE] [HKR] [HKR] [HKR] [AILMFWVYGSTCPNQDE] [HKR] [AI  
L3 0 S L2 AND SQL=18

FILE 'HCAPLUS' ENTERED AT 11:26:52 ON 02 JUL 2007

L4 7 S L2